

TGFb+MMP+iln b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
ATGCGCGCT	CCGCGCTCG	GCTGCTGCG	CTGCTGCTAC	CGCTGCTG	GCTACTGCTG	60
MetProProS	erGlyLeuAr	gLeuLeuPro	LeuLeuLeuP	roLeuLeuTr	pLeuLeuVal	
CTGAGCGCTG	GCGCGCTG	CGCGGACTA	TCCAGCTGCA	AGACTATCGA	CATGGAGCTG	120
LeuThrProG	lyProProAl	aAlaGlyLeu	SerThrCysL	ysThrIleAs	pMetGluLeu	
GTTAGCGGGA	AGCGCATGGA	GCCCATCGCG	GCCAGATCC	TGTCCAAGCT	GCGGCTCGCC	180
VallLysArgL	ysArgIleGl	uAlaIleArg	GlyGlnIleL	euSerLysLe	uArgLeuAla	
AGCGCGCGGA	GCGAGGCGGA	GCTGCGCGCC	GCGCGCTGCG	CGAGGCGCT	GCTCGCGCTG	240
SerProProS	erGlnGlyGl	uValProPro	GlyProLeuP	roGluAlaVa	lLeuAlaLeu	
TACAACAGCA	CCCGCGACG	GCTGCGCGCG	GAGAGTCCAG	AACCGAGGCC	CGAGCGCTGAG	300
TyrAsnSerT	hrArgAspAr	gValAlaGly	GluSerAlaG	luProGluPr	oGluProGlu	
GCGACTACT	ACGCGACGGA	GCTCACCGCG	GTCCTAATGG	TGGAAACCCA	CAACGAAATC	360
AlaAspTyrT	yrAlaLysGl	uValThrArg	ValLeuMetV	alGluThrHi	sAsnGluIle	
TATGACAAGT	TCAAGCAGAG	TACACACAGC	ATATATATGT	TCTTCAACAC	ATCAGAGCTC	420
TyrAspLysP	heLysGlnSe	rThrHisSer	IleTyrMetP	hePheAsnTh	rSerGluLeu	
CGAGAAGCGG	TACCTGAACC	CGTGTGCTC	TCCCGGCGAG	AGCTGGCTCT	GCTGAGGAGG	480
ArgGluAlaV	alProGluPr	oValLeuLeu	SerArgAlaG	luLeuArgLe	uLeuArgArg	
CTCAAGTTAA	AAGTGGAGCA	GCACTGGAG	CTGTACCAGA	AATACAGCAA	CAATTCCTGG	540
LeuLysLeuL	ysValGluGl	nHisValGlu	LeuTyrGlnL	ysTyrSerAs	nAsnSerTrp	
CGATACTCA	GCAACCGGCT	GCTGGCACCC	AGCGACTGCG	CAGAGTGGTT	ATCTTTTGAT	600
ArgTyrLeuS	erAsnArgLe	uLeuAlaPro	SerAspSerP	roGluTrpLe	uSerPheAsp	
GTCACCGGAG	TGTGCGGCA	GTCGTTGAGC	CGTGGAGGGG	AAATTCAGGG	CITTCGCCIT	660
ValThrGlyV	alValArgGl	nTrpLeuSer	ArgGlyGlyG	luIleGluGl	yPheArgLeu	
AGCGCGCACT	GCTCGCTGGA	CAGCAGGAT	AACACACTGC	AAGTGGACAT	CAACGGGTTC	720
SerAlaHisC	ysSerCysAs	pSerArgAsp	AsnThrLeuG	InValAspIl	eAsnGlyPhe	
ACTACCGGCC	GCGAGGTTGA	CCTGGCCACC	ATTATGCGCA	TGAACCGGCC	TTTCTGCTT	780
ThrThrGlyA	rgArgGlyAs	pLeuAlaThr	IleHisGlyM	etAsnArgPr	oPheLeuLeu	
CTCATGGCCA	CCCGCTGGA	GAGGCGCCAG	CATCTGCAAA	GCGAATTCGG	GCGAGGCGGA	840
LeuMetAlaT	hrProLeuGl	uArgAlaGln	HisLeuGlnS	erGluPheGl	yGlyGlyGly	
TCCCGGCTCG	GCTTTGGGC	GCGAGGCGGC	TCAAGCGCGG	CAATCAACTA	TAAGCAGCTC	900
SerProLeuG	lyLeuTrpAl	aglyGlyGly	SerAlaAlaA	laIleAsnTy	rLysGlnLeu	
CAGCTCCAG	AAAGCAAGAA	CATTGGGAAA	TGTCAGGAGC	TCTTGGAGCA	GCTGAATGGA	960
GlnLeuGlnG	luArgThrAs	nIleArgLys	CysGlnGluL	euLeuGluGl	nLeuAsnGly	

Fig. 1

095633-073004

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
AAGATCAACC	TCAOCTACAG	GGGGGACTTC	AAGATCCCTA	TGGAGATGAC	GGAGAAGATG	1020
LysIleAsnL	euThrTyrAr	gAlaAspPhe	LysIleProM	etGluMetTh	rGluLysMet	
CAGAAGAGTT	ACACTGCCIT	TGCCATOCOA	GAGATGCTCC	AGAATGCTCT	TCTTGICTTC	1080
GlnLysSerT	yrThrAlaPh	eAlaIleGln	GluMetLeuG	lnAsnValPh	eLeuValPhe	
AGAAACAATT	TCTOCAGCAC	TGGGTGGAAT	GAGACTATTG	TTGTAGTCT	CCTGGATGAA	1140
ArgAsnAsnP	heSerSerTh	rGlyTrpAsn	GluThrIleV	alValArgLe	uLeuAspGlu	
CTCACACAGC	AGACAGTGTT	TCTGAAGACA	GTACTAGAGG	AAAAGCAAGA	GGAAAGATTG	1200
LeuHisGlnG	lnThrValPh	eLeuLysThr	ValLeuGluG	luLysGlnGl	uGluArgLeu	
AAGTGGGAGA	TGTCCTCAAC	TGCTCTOCAC	TTGAAGAGCT	ATTACTGGAG	GGTGCAAAGG	1260
ThrTrpGluM	etSerSerTh	rAlaLeuHis	LeuLysSerT	yrTyrTrpAr	gValGlnArg	
TACCTTAAAC	TCATGAAGTA	CAACAGCTAC	GCTTGGATGG	TGGTCCGAGC	AGAGATCTTC	1320
TyrLeuLysL	euMetLysTy	rAsnSerTyr	AlaTrpMetV	alValArgAl	aGluIlePhe	
AGGAACCTTC	TCATCATTCG	AAGACTTACC	AGAACTTCC	AAAACIGATC	TAGACC	1376
ArgAsnPheL	euIleIleAr	gArgLeuThr	ArgAsnPheG	lnAsn...Se	rArg	
				uga		

09756283 - 073004

60

Fig. 2

ifn+MMP+TGFB Sequence

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GTGTTGCTCT	CCCGGGCAGA	GCTGGCTCTG	CTGAGGAGGC	TCAAGTTAAA	AGTGGAGCAG	1020
ValLeuLeuS	erArgAlaGl	uLeuArgLeu	LeuArgArgL	euLysLeuLy	sValGluGln	
CACGTGGAGC	TGTACAGAA	ATACAGCAAC	AATTCCTGGC	GATAOCTCAG	CAACGGGCTG	1080
HisValGluL	euTyrGlnLy	sTyrSerAsn	AsnSerTrpA	rgTyrLeuSe	rAsnArgLeu	
CTGGCAOCCA	GCGACTGGCC	AGAGTGGTTA	TCTTTTGATG	TCACGGGAGT	TGTCGGGCAG	1140
LeuAlaProS	erAspSerPr	oGluTrpLeu	SerPheAspV	alThrGlyVa	lValArgGln	
TGGTTGAGCC	GTGGAGGGGA	AATTGAGGGC	TTTGGCTTCA	GCGOCCACTG	CTCTGTGAC	1200
TrpLeuSerA	rgGlyGlyGl	uTleGluGly	PheArgLeuS	erAlaHisCy	sSerCysAsp	
AGCAGGGATA	ACACACTGCA	AGTGGACATC	AACGGGTTC	CTACCGGCGG	CCGAGGTGAC	1260
SerArgAspA	snThrLeuGl	nValAspIle	AsnGlyPheT	hrThrGlyAr	gArgGlyAsp	
CTGGCACCA	TTCATGGCAT	GAACGGGCT	TTCCTGCTTC	TCATGGGCAC	CCGCTGGAG	1320
LeuAlaThrI	leHisGlyMe	tAsnArgPro	PheLeuLeuL	euMetAlaTh	rProLeuGlu	
AGGGGCCAGC	ATCTGCAAAG	CtgaTCTAGA	CC			1352
ArgAlaGlnH	isLeuGlnSe	r...SerArg				

09756393-073004

	1	20	↓	40	60
Hu TGF-β 1	MPPSGRLRLPLLLPLLV-LTPGPPAAGLSCTIDHMLVKKRIEAI	RGQILSKLRASPPSGE	VP-PGP		
Hu TGF-β 2	MHYCVLSAFLILH	LVTVAL-----SLSTCSTLDHMOFMKKRIEAI	RGQILSKLKLTSPP	---EDYPEPEE	
Hu TGF-β 3	MKMHLOALVVLALLNFATVSL-----SLSTCTLD	FGHIKKRVEAIRGOILSKLR	LTSP	---EPTV-MTH	
Ck TGF-β 4	-----	-----	-----	-----	-----
Fg TGF-β 5	MEV-----LWMLLVLLV-LHSSLSLSTCKAVDH	EEVKKRIEAI	RGQILSKLKLDPDVS	EK-MTV	
	+	+	++	+++	+
	80		100		120
Hu TGF-β 1	LPEAVLALYNSTRORVAGESAEPE-PEP-----EADYYAKEVIRVLHV----	ETHNEIYDKFKQSTHSIYHFF			
Hu TGF-β 2	VPPEVISIYNSTRDLL--DEKASR-RAAACERERSOEYYAKEVYKIDMPPFFPS-EHAIPPTFYRYP-FRIVRF				
Hu TGF-β 3	VPYQVLAALYNSTRELL--EENGER-KEEGCTOENTESEYYAKEIHKFDMIOGLAE-HNELAVCPKGIT-SKVRF				
Ck TGF-β 4	-----M--DPMSIGPK--SCG-----	-----GSPW-RPP-GTAPWSIG-SR--RA			
Fg TGF-β 5	PSEAI-F-LYNSTILE-VIREKATRE-EEHVGHODHIOYYAKOVYRF----	ESITELEDHEFKF-----F			
	++++		+++		
	140		160		180
Hu TGF-β 1	NTSEL-----RE-AVPEPVLLS-RAELRLRLKL----	KV-EOHVELYQ-----KYSNHSURYLSNRL	LAPSDSPE		
Hu TGF-β 2	DVSA-----MEKNASHLV-KAEFRVRLWPK-ARVPEORIELYQILSKDLSPTORYIDSKVVKTRAEGE				
Hu TGF-β 3	NYSS-----VEKNRTNLF-RAEFRVLRVPNS-SKRNEQRIELFOILRP-DEHIAKORYIGGKNLPTRGTAE				
Ck TGF-β 4	TASSCSTSSRVRAEVGGRALLHRAELRHLROKAAADSAGTEORLELYOGYG----	NASURYLHGRSVRATAODE			
Fg TGF-β 5	NASHV-----RENVGMW-SLLH-HAELRHYK-KOTD--KNMDORMELFW--KYOENGITHSRYLESKYITPVTOOE				
	+	+	++	+	+
	200		220		240
Hu TGF-β 1	WLSFDVTGVVQWLSRGGEIEGFRLSAHCSG-----DSRDNTLOVDIN-GFTTGR-----RGDLATJ)-----				
Hu TGF-β 2	WLSFDVTOAVHEWLNHKNRNLGFKISLHCPCTFVPSNHYIIPNKSEELARFA-GIDGISTYISGOOKTIKSTRK				
Hu TGF-β 3	WLSFDVTDIVREWLLRRESNLGLEISIHCPCHTFOP-NGDILENIHEVMEIKFK-GVONEDDHGRGQIGRLK---K				
Ck TGF-β 4	WLSFDVTOAVHOWLSGSELLGVFKLSVHCPCEMGP-GHADENRISIEGFEOQ-----RGDHOSIA---K				
Fg TGF-β 5	WMSFDVTKIVNEWLKRAEENEQFGLPAKCK-----PTPOAKD-----IDIEGFPAL-RGDLASL--SSK				
	+++++	+	++	+	++
	260		↓ 280		300
Hu TGF-β 1	----HGMHRPFLLLHATPLERA-OK--LQSS---RHRRALDTHYCFSS--EKNCCVROLYIDFRKDLGWKWIHEP				
Hu TGF-β 2	KNSGKT---PHLLHLLPSYRL-ESQ-----QINRRKKRALDAAYCFRNV--ODNCCLRPLYIDFRKDLGWKWIHEP				
Hu TGF-β 3	OKONN--N-PHLILHMIPPHRL-DNPGOGGQ---RKKRALDTHYCFRNL--EENCCVRPLYIDFRDLGWKWIHEP				
Ck TGF-β 4	-KRRR--V-PYVLAHALPAERANE--LHSA---RRRROLDTDYCFGPGTDEKNCCVRPLYIDFRKDLGWKWIHEP				
Fg TGF-β 5	ENT-----KPYL--HITSHPAERIDTIVTSS---RKKRGVGOEYCFGNN--GNCCVKPLYINFRKDLGWKWIHEP				
	+	+	+	+++	+++
	320		340		360
Hu TGF-β 1	KGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNHIVRSCKCS				
Hu TGF-β 2	KGYHANFCAGACPYLWSSDTQHSRVLSTYNTINPEASASPCCVSODLEPLTILYYIGKTPKIEQLSNHIVKSCCKCS				
Hu TGF-β 3	KGYHANFCGCPYLRSDTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS				
Ck TGF-β 4	KGYHANFCGCPYIWSADTOTIKVLALYNQHNPGASAAPCCVPQDLPPIIYVGRNVRVEQLSNHVVRSCKCS				
Fg TGF-β 5	KGYEANYCLGNCPIYWSMDTQYSKVLALYNQHNPGASISPCCVPDVLPLPIIYVGRVIAKVEQLSNHVVRSCKCS				
	+++	+++	+++	+++	+++

Fig. 3

Protein	Sequence	Reference
MMP-1/MMP-8		
Human type I collagen ($\alpha 1$)	Ala-Pro-Gln-Gly ₇₇₅ ~Ile ₇₇₆ -Ala-Gly-Gln	80
Human type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₅ ~Leu ₇₇₆ -Leu-Gly-Ala	80
Human type II collagen	Gly-Pro-Gln-Gly ₇₇₅ ~Leu ₇₇₆ -Ala-Gly-Gln	80
Human type III collagen	Gly-Pro-Leu-Gly ₇₇₅ ~Ile ₇₇₆ -Ala-Gly-Ile	80
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₇₉ ~Leu ₆₈₀ -Arg-Val-Gly	84
Rat α_2 -macroglobulin	Ala-Ala-Tyr-His ₆₈₁ ~Leu ₆₈₂ -Val-Ser-Gln	84
Rat α_2 -macroglobulin	Met-Asp-Ala-Phe ₆₉₁ ~Leu ₆₉₂ -Glu-Ser-Ser	84
Rat α_1 -macroglobulin	Glu-Pro-Gln-Ala ₆₈₃ ~Leu ₆₈₄ -Ala-Met-Ser	84
Rat α_1 -macroglobulin	Gln-Ala-Leu-Ala ₆₈₅ ~Met ₆₈₆ -Ser-Ala-Ile	84
Chicken ovostatin	Pro-Ser-Tyr-Phe ₆₇₃ ~Leu ₆₇₄ -Asn-Ala-Gly	79
Human pregnancy zone protein	Tyr-Glu-Ala-Gly ₆₈₅ ~Leu ₆₈₆ -Gly-Val-Val	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₆₈₇ ~Val ₆₈₈ -Val-Glu-Arg	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly ₇₅₇ ~Ile ₇₅₈ -Ser-Ser-Thr	84
α_1 -Protease inhibitor	Gly-Ala-Met-Phe ₃₅₂ ~Leu ₃₅₃ -Glu-Ala-Ile	85
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	86
Human aggrecan	Thr-Glu-Gly-Glu ₃₇₃ ~Ala ₃₇₄ -Arg-Gly-Ser	86
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₉ ~Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-2		
Guinea pig $\alpha 1$ (I) gelatin	Gly-Ala-Hyp-Gly ₃₄₇ ~Leu ₃₄₈ -Glx-Gly-His	24
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Gln-Gly ₁₉₀ ~Val ₁₉₁ -Arg-Gly-Glu	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₂₇₇ ~Val ₂₇₈ -Gln-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ser-Gly ₃₀₁ ~Leu ₃₀₂ -Hyp-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₃₃₁ ~Glu ₃₃₂ -Arg-Gly-Ser	30
Rat $\alpha 1$ (I) gelatin	Gly-Ala-Lys-Gly ₃₆₁ ~Leu ₃₆₂ -Thr-Gly-Ser	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₃₈₂ ~Gln ₃₈₃ -Asp-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ala-Gly ₆₃₄ ~Phe ₆₃₅ -Ala-Gly-Pro	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Ile-Gly ₆₇₆ ~Asn ₆₇₇ -Val-Gly-Ala	30
Rat $\alpha 1$ (I) gelatin	Gly-Pro-Hyl-Gly ₆₈₅ ~Ser ₆₈₆ -Arg-Gly-Ala	30
Bovine type I collagen ($\alpha 1$)	Gly-Pro-Gln-Gly ₇₇₅ ~Ile ₇₇₆ -Ala-Gly-Gln	22
Bovine type I collagen ($\alpha 2$)	Gly-Pro-Gln-Gly ₇₇₅ ~Leu ₇₇₆ -Leu-Gly-Ala	22
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₄₃ ~Tyr ₆₁ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87
Human insulin-like growth factor binding protein-3	Leu-Arg-Ala-Tyr ₉₉ ~Leu ₁₀₀ -Leu-Pro-Ala	88
MMP-3		
Human α_2 -macroglobulin	Gly-Pro-Glu-Gly ₆₇₉ ~Leu ₆₈₀ -Arg-Val-Gly	79
Human α_2 -macroglobulin	Arg-Val-Gly-Phe ₆₈₄ ~Tyr ₆₈₅ -Glu-Ser-Asp	79
Human α_1 -antichymotrypsin	Leu-Leu-Ser-Ala ₃₆₀ ~Leu ₃₆₁ -Val-Glu-Thr	91
α_1 -protease inhibitor	Glu-Ala-Ile-Pro ₃₃₇ ~Met ₃₃₈ -Ser-Ile-Pro	91
Aotithrombin III	Ile-Ala-Gly-Arg ₃₈₅ ~Ser ₃₈₆ -Leu-Asn-Pro	91
Chicken ovostatin	Leu-Asn-Ala-Gly ₆₇₇ ~Phe ₆₇₈ -Thr-Ala-Ser	79, 92
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	93
Substance P	Lys-Pro-Gln-Gln ₆ ~Phe ₇ -Phe-Gly-Leu	37
Human ProMMP-1	Asp-Val-Ala-Gln ₈₀ ~Phe ₈₁ -Val-Leu-Thr	43
Human ProMMP-3	Asp-Thr-Leu-Glu ₆₈ ~Val ₆₉ -Met-Arg-Lys	94
Human ProMMP-3	Asp-Val-Gly-His ₈₂ ~Phe ₈₃ -Arg-Thr-Phe	94
Human ProMMP-8	Asp-Ser-Gly-Gly ₇₈ ~Phe ₇₉ -Met-Leu-Thr	95
Human ProMMP-9	Arg-Val-Ala-Glu ₄₀ ~Met ₄₁ -Arg-Gly-Glu	48
Human ProMMP-9	Asp-Leu-Gly-Arg ₈₇ ~Phe ₈₈ -Gln-Thr-Phe	48
Human fibronectin	Pro-Phe-Ser-Pro ₆₈₉ ~Leu ₆₉₀ -Val-Ala-Thr	21

Fig. 4

	Sequence	Reference
Human insulin-like growth factor	Leu-Arg-Ala-Tyr ₉₀ ~Leu ₁₀₀ -Leu-Pro-Ala	88
Binding protein-3	Ala-Pro-Gly-Asn ₁₀₉ ~Ala ₁₁₀ -Ser-Glu-Ser	88
	Phe-Ser-Ser-Glu ₁₇₆ ~Ser ₁₇₇ -Lys-Arg-Glu	88
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Ala-Gly-Gly-Ala ₁₁₅ ~Gln ₁₁₆ -Met-Gly-Val	96
Bovine $\alpha 1$ (II) collagen, N-telopeptide	Gln-Met-Gly-Val ₁₁₉ ~Met ₁₂₀ -Gln-Gly-Pro	96
Bovine $\alpha 1$ (IX) collagen, NC2	Met-Ala-Ala-Ser~Leu-Lys-Arg-Pro	96
Bovine $\alpha 2$ (IX) collagen, NC2	~Ala-Lys-Arg-Glu	96
Bovine $\alpha 3$ (IX) collagen, NC2	~Leu-Arg-Lys-Pro	96
Bovine $\alpha 1$ (XI) collagen, N-telopeptide	Gln-Ala-Gln-Ala~Ile-Leu-Gln-Gln	96
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Bovine insulin, B chain	Leu-Val-Glu-Ala ₁₄ ~Leu ₁₅ -Tyr-Leu-Val	97
Bovine insulin, B chain	Glu-Ala-Leu-Tyr ₁₆ ~Leu ₁₇ -Val-Cys-Gly	21, 97
MMP-7		
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87
Human prourokinase	Pro-Pro-Glu-Glu ₁₄₃ ~Leu ₁₄₄ -Lys-Phe-Gln	98
MMP-9		
Human type V collagen ($\alpha 1$)	Gly-Pro-Pro-Gly ₄₃₉ ~Val ₄₄₀ -Val-Gly-Pro	99
Human type V collagen ($\alpha 2$)	Gly-Pro-Pro-Gly ₄₄₅ ~Leu ₄₄₆ -Arg-Gly-Glu	99
Human type XI collagen ($\alpha 1$)	Gly-Pro-Gly-Gly ₄₃₉ ~Val ₄₄₀ -Val-Gly-Pro	99
Human aggrecan	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala ₆₂ ~Tyr ₆₃ -His-Gly-Ala	90
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
MMP-10		
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~Ile ₁₇ -Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87

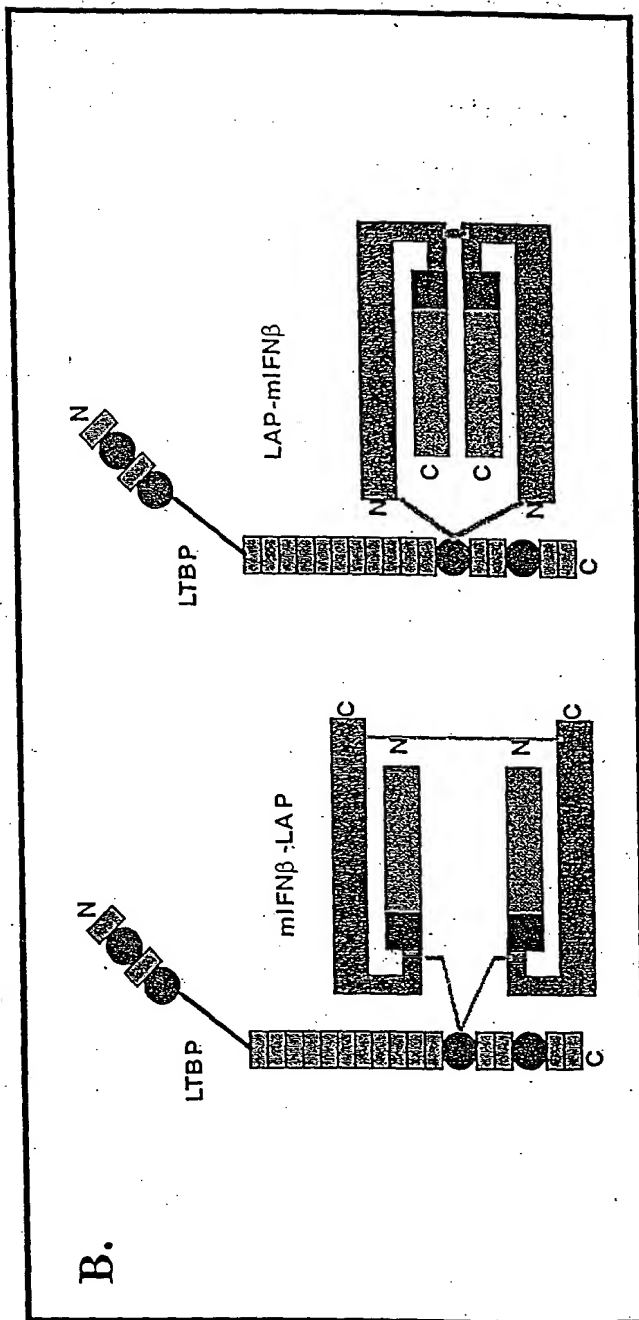
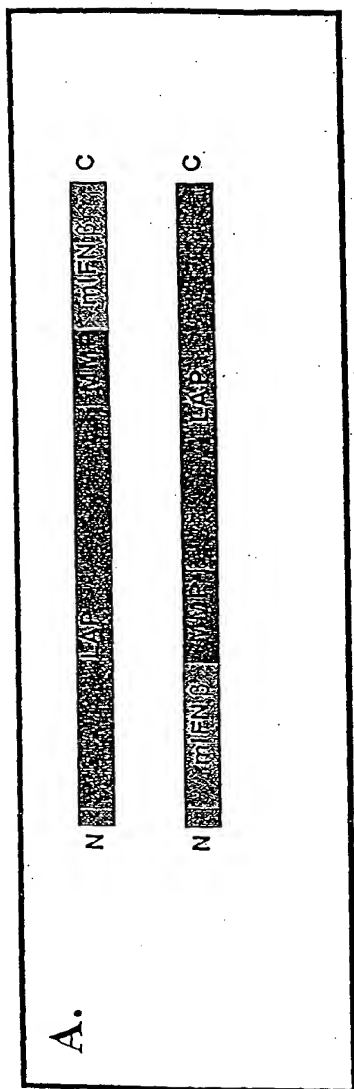


FIG. 5

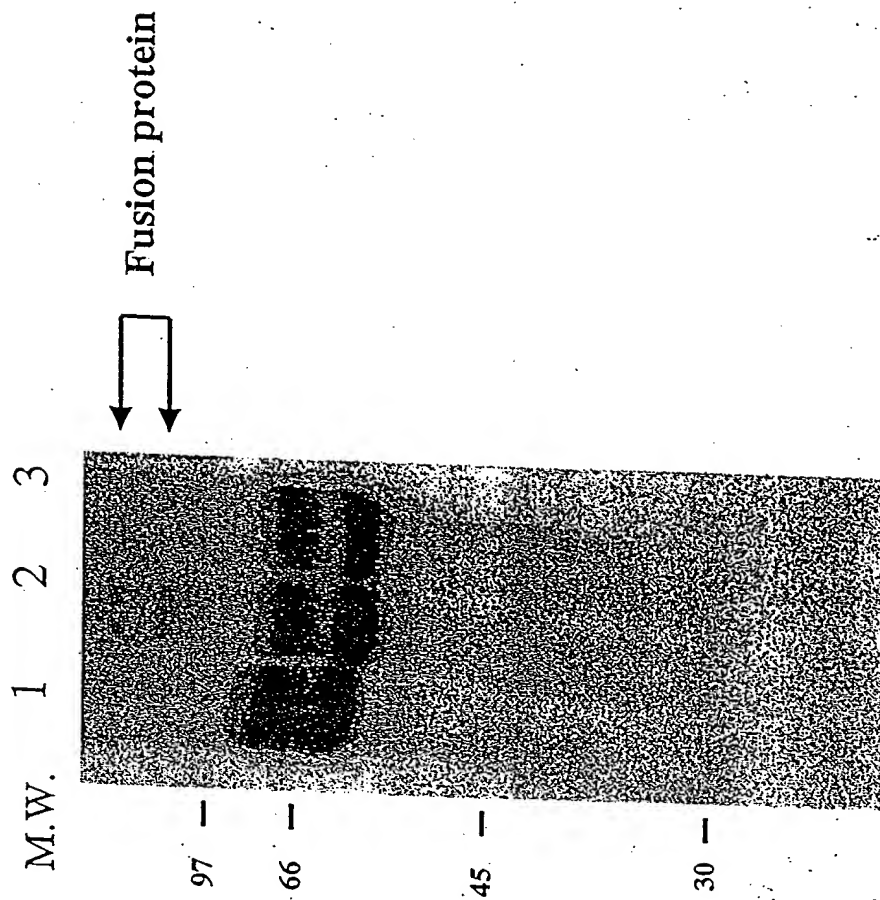


Fig. 6

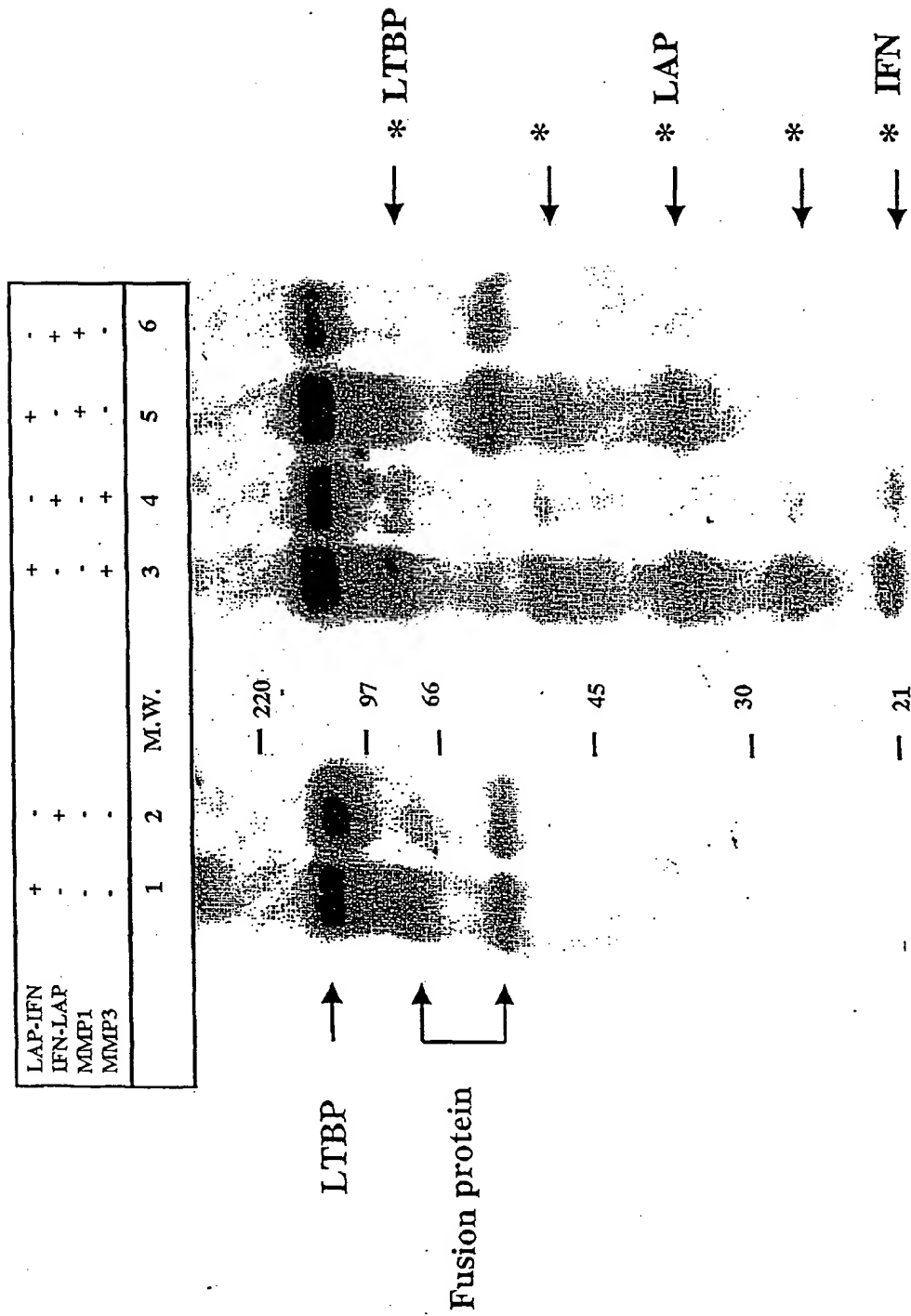


Fig. 7

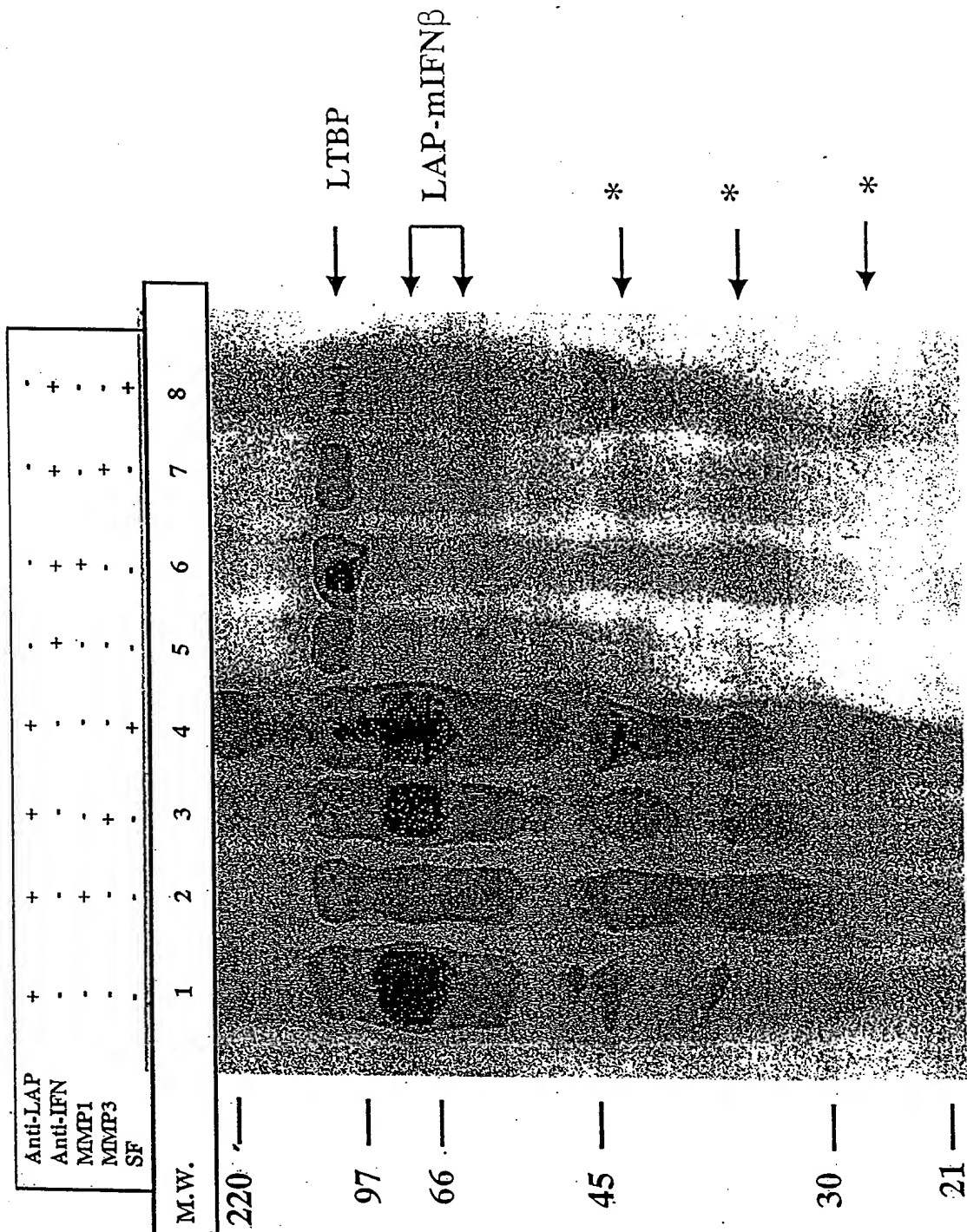


Fig. 8a

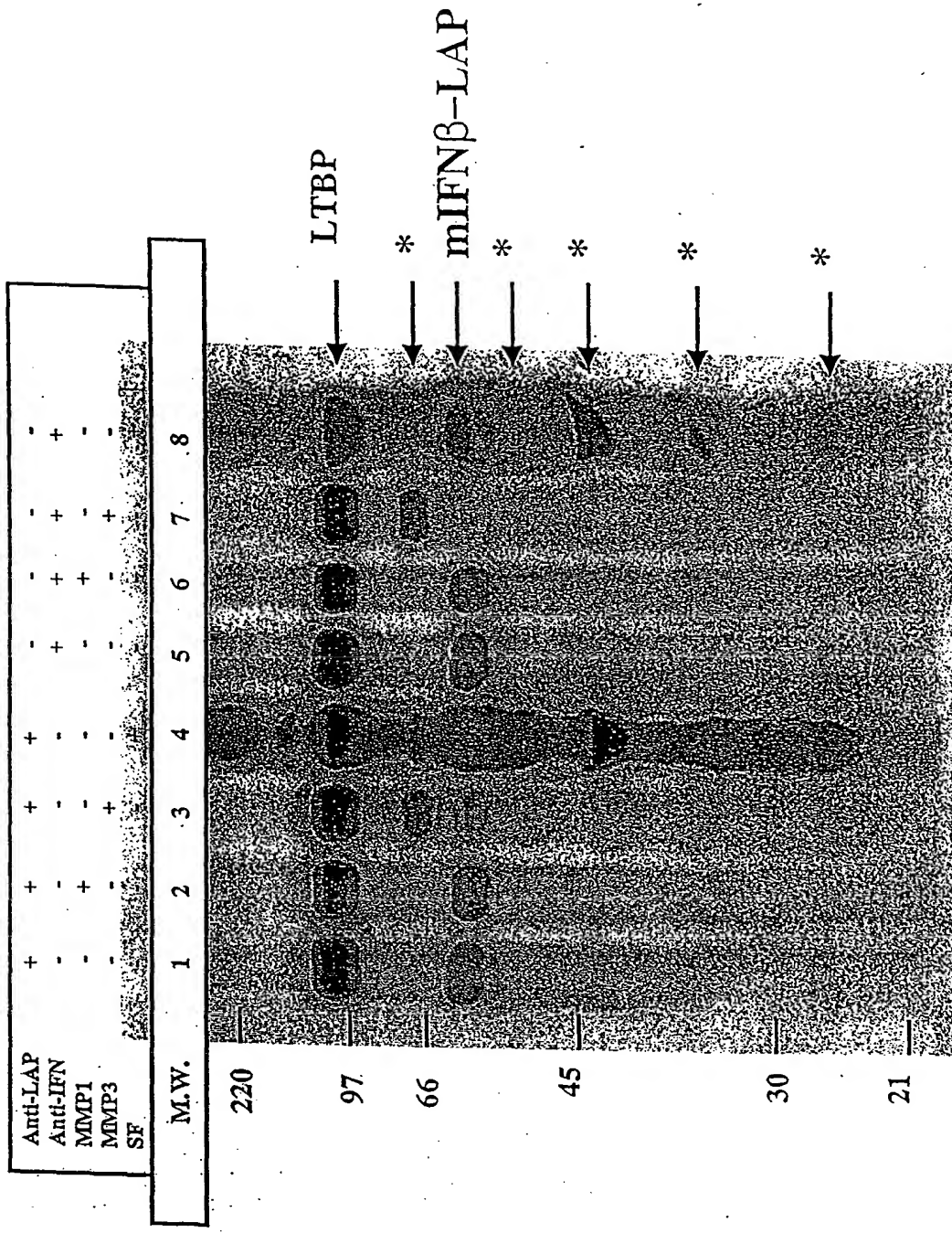


Fig. 8b

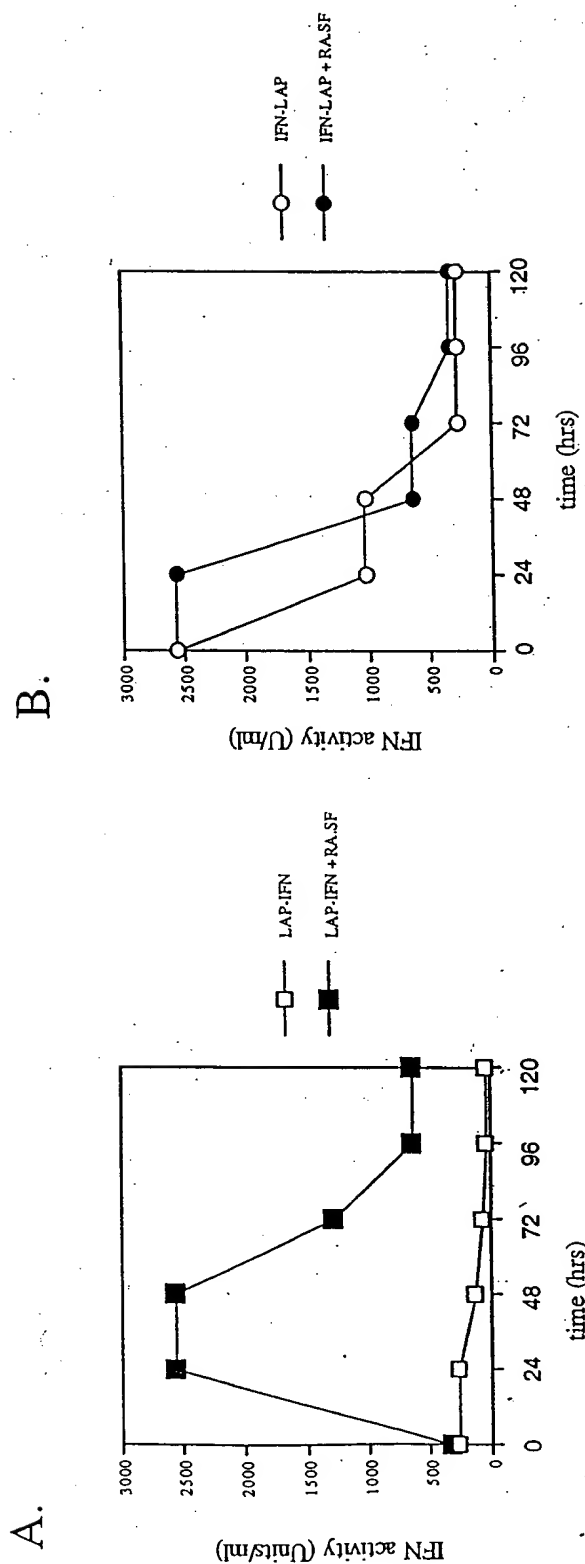
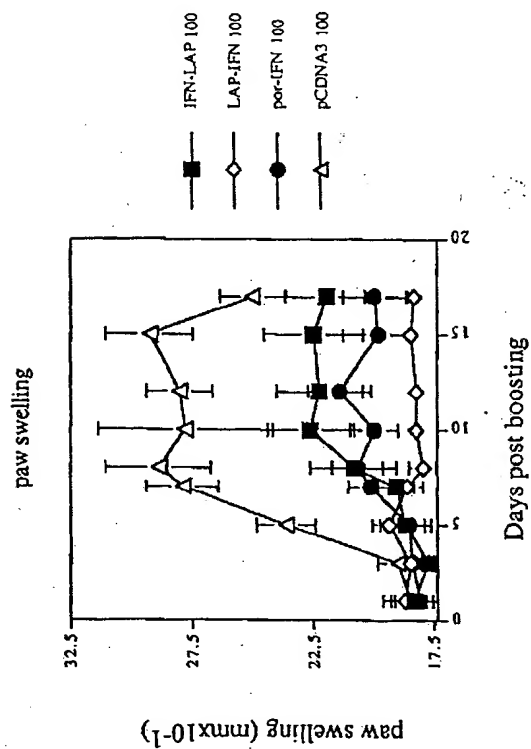


Fig. 9

A.



B.

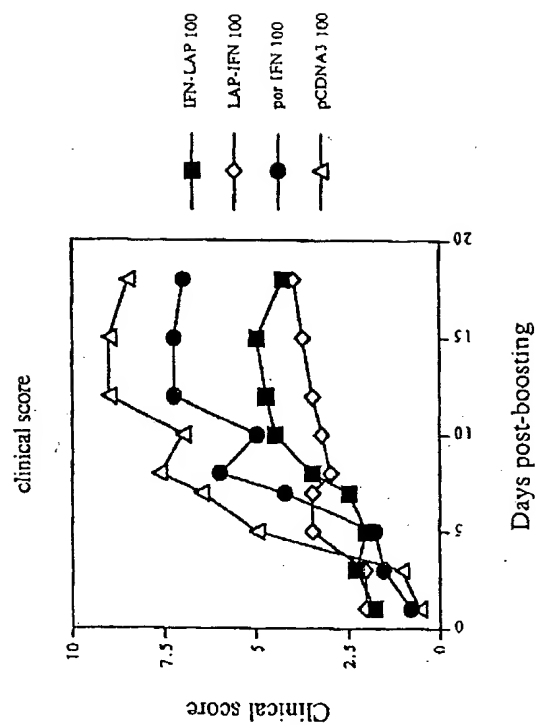


Fig. 10